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RAW SEQUENCE LISTING   DATE: 03/18/2002
PATENT APPLICATION: US/09/931,007A   TIME: 15:35:21

Input Set : A:\EP.txt
Output Set: N:\CRF3\03182002\I931007A.raw

```
 3 <110> APPLICANT: Aventis Pharma S.A.
 5 <120> TITLE OF INVENTION: SYSTEM FOR REGULATING IN VIVO THE EXPRESSION OF A TRANSGENE
BY
 6       CONDITIONAL INHIBITION
 8 <130> FILE REFERENCE: 03806.0512
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/931,007A
C--> 10 <141> CURRENT FILING DATE: 2001-08-17
10 <150> PRIOR APPLICATION NUMBER: FR 00/10730
11 <151> PRIOR FILING DATE: 2000-08-18
13 <150> PRIOR APPLICATION NUMBER: US 60/239,246
14 <151> PRIOR FILING DATE: 2000-10-11
16 <160> NUMBER OF SEQ ID NOS: 11
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 688
22 <212> TYPE: PRT
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
W--> 26 <221> NAME/KEY: misc
27 <222> LOCATION: (1)..(688)
28 <223> OTHER INFORMATION: Sequence for PPAR-gamma-2-gamma-2, a modified human PPAR-
gamma (P
29       eroxisome Proliferator Activated Receptor-gamma)
32 <400> SEQUENCE: 1
34 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
35 1               5                   10                  15
37 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
38              20                  25                  30
40 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
41          35                  40                  45
43 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
44      50                  55                  60
46 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
47 65                  70                  75                  80
49 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
50                  85                  90                  95
52 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
53              100                 105                 110
55 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Arg Asn Lys Cys
56          115                 120                 125
58 Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
59      130                 135                 140
61 Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu
62 145                 150                 155                 160
```

64 Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp

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```
65                 165              170              175
67 Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe
68             180              185              190
70 Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr
71         195              200              205
73 Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly
74     210              215              220
76 Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser
77 225              230              235              240
79 Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val
80             245              250              255
82 Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe
83             260              265              270
85 Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val
86         275              280              285
88 His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly
89     290              295              300
91 Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys
92 305              310              315              320
94 Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe
95             325              330              335
97 Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile
98             340              345              350
100 Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn
101         355              360              365
103 Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
104     370              375              380
106 Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys
107 385              390              395              400
109 Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val
110             405              410              415
112 Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His
113         420              425              430
115 Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr Ala Trp Ala Ile Leu
116         435              440              445
118 Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn
119     450              455              460
121 Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro
122 465              470              475              480
124 Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys
125             485              490              495
127 Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys
128         500              505              510
130 Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu
131         515              520              525
133 Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu
134     530              535              540
136 Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr
137 545              550              555              560
```

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```
139 Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu
140             565                 570             575
142 Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp
143         580                 585             590
145 Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg
146         595                 600             605
148 Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu
149     610                 615             620
151 Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser
152 625                 630             635                 640
154 Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile
155             645                 650             655
157 Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr
158             660                 665             670
160 Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
161         675                 680             685
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 19
165 <212> TYPE: DNA
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C--> 166 <213> ORGANISM: Artificial
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168 <220> FEATURE:
169 <223> OTHER INFORMATION: PPAR binding site
171 <400> SEQUENCE: 2
172 tcaaccttta ccctggtag                                       19
175 <210> SEQ ID NO: 3
176 <211> LENGTH: 13
177 <212> TYPE: DNA
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C--> 178 <213> ORGANISM: Artificial
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180 <220> FEATURE:
181 <223> OTHER INFORMATION: PPAR binding site
183 <400> SEQUENCE: 3
184 aggtcaaagg tca                                             13
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 30
189 <212> TYPE: DNA
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C--> 190 <213> ORGANISM: Artificial
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192 <220> FEATURE:
193 <223> OTHER INFORMATION: primer
195 <400> SEQUENCE: 4
196 atgcatcgat ggccgcttcg agcagacatg                           30
199 <210> SEQ ID NO: 5
200 <211> LENGTH: 39
201 <212> TYPE: DNA
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C--> 202 <213> ORGANISM: Artificial
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204 <220> FEATURE:
205 <223> OTHER INFORMATION: primer
207 <400> SEQUENCE: 5
208 atgcgtcgac tctagccgat tttaccacat ttgtagagg                 39
211 <210> SEQ ID NO: 6
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      212 <211> LENGTH: 33
      213 <212> TYPE: DNA
C--> 214 <213> ORGANISM: Artificial
      216 <220> FEATURE:
      217 <223> OTHER INFORMATION: primer
      219 <400> SEQUENCE: 6
      220 cgagcatgct gctgctgctg ctgctgctgg gcc                       33
      223 <210> SEQ ID NO: 7
      224 <211> LENGTH: 33
      225 <212> TYPE: DNA
C--> 226 <213> ORGANISM: Artificial
      228 <220> FEATURE:
      229 <223> OTHER INFORMATION: primer
      231 <400> SEQUENCE: 7
      232 gggtctagat taacccgggt gcgcggcgtc ggt                       33
      235 <210> SEQ ID NO: 8
      236 <211> LENGTH: 20
      237 <212> TYPE: DNA
C--> 238 <213> ORGANISM: Artificial
      240 <220> FEATURE:
      241 <223> OTHER INFORMATION: primer
      243 <400> SEQUENCE: 8
      244 cgatcatgtt cgacgacgcc                                      20
      247 <210> SEQ ID NO: 9
      248 <211> LENGTH: 20
      249 <212> TYPE: DNA
C--> 250 <213> ORGANISM: Artificial
      252 <220> FEATURE:
      253 <223> OTHER INFORMATION: primer
      255 <400> SEQUENCE: 9
      256 ccaggtcgca ggcggtgtag                                      20
      259 <210> SEQ ID NO: 10
      260 <211> LENGTH: 23
      261 <212> TYPE: RNA
C--> 262 <213> ORGANISM: Artificial
      264 <220> FEATURE:
      265 <223> OTHER INFORMATION: aptamer
      267 <400> SEQUENCE: 10
      268 ggccugggcg agaaguuuag gcc                                  23
      271 <210> SEQ ID NO: 11
      272 <211> LENGTH: 72
      273 <212> TYPE: RNA
C--> 274 <213> ORGANISM: Artificial
      276 <220> FEATURE:
      277 <223> OTHER INFORMATION: aptamer
      279 <400> SEQUENCE: 11
      280 ggugaucaga uucggaucca auguuaugcu ucucugccug ggaacagcug ccugaagcuu   60
      282 uggauccguc gc                                             72
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VERIFICATION SUMMARY   DATE: 03/18/2002
PATENT APPLICATION: **US/09/931,007A**   TIME: 15:35:23

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:166 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:178 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:190 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:202 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:214 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:226 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:238 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:250 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:262 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:274 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
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